

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:16:08 ; Search time 172.18 Seconds  
(without alignments)  
51.241 Million cell updates/sec

Title: US-09-052-089A-6

Perfect score: 293  
Sequence: 1 LSLCTICSDFFDHSRDVAAL.....IQMFETAPSRTPCQRIOVG 51

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_19:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	293	100.0	470	11	008854	008854 mus musculu
2	286	97.6	223	11	0922M8	0922M8 mus musculu
3	286	97.6	469	4	Q9BWF2	Q9BWF2 homo sapien
4	286	97.6	470	11	Q9CP4	Q9CP4 mus musculu
5	272	92.8	469	4	000467	000467 homo sapien
6	244	83.3	433	13	Q9YGN2	Q9YGN2 figu rubrip
7	128	43.7	435	5	Q95SS5	Q95SS5 drosophila
8	128	43.7	455	5	Q9V8D7	Q9V8D7 drosophila
9	127	43.3	310	10	082372	082372 arabidopsis
10	127	43.3	420	4	075866	075866 homo sapien
11	125	42.7	325	10	Q9M9U8	Q9M9U8 arabidopsis
12	124.5	42.5	263	5	Q95RB5	Q95RB5 drosophila
13	123	42.0	158	5	Q9XZS4	Q9XZS4 drosophila
14	115	39.2	327	11	Q9DAH2	Q9DAH2 mus musculu
15	115	39.2	349	10	Q947X9	Q947X9 oryza sativ
16	114	38.9	181	5	097260	097260 plasmodium

17	113	38.6	224	10	Q9M9U7	Q9M9U7 arabidopsis
18	113	38.6	386	10	Q9LT14	Q9LT14 arabidopsis
19	112	38.2	304	5	Q9N3D1	Q9N3D1 caenorhabdi
20	112	38.2	344	10	065594	065594 arabidopsis
21	112	38.2	368	10	Q944T9	Q944T9 arabidopsis
22	112	38.2	383	10	Q9LMT3	Q9LMT3 arabidopsis
23	112	38.2	621	5	Q9V9T8	Q9V9T8 drosophila
24	112	38.2	626	5	Q95SP2	Q95SP2 drosophila
25	111	37.9	325	10	Q9LTU8	Q9LTU8 arabidopsis
26	110	37.5	274	10	Q9LZ10	Q9LZ10 arabidopsis
27	108	36.9	230	10	Q9FN35	Q9FN35 arabidopsis
28	108	36.9	489	5	Q9XUM8	Q9XUM8 caenorhabdi
29	107	36.5	137	4	Q9NSR1	Q9NSR1 homo sapien
30	107	36.5	396	10	Q9FM98	Q9FM98 arabidopsis
31	107	36.5	551	3	Q9M109	Q9M109 saccharomyc
32	107	36.5	879	13	Q90ZT8	Q90ZT8 gallus gall
33	107	36.5	923	13	Q90ZT7	Q90ZT7 xenopus lae
34	107	36.5	989	11	Q99ML9	Q99ML9 mus musculu
35	106.5	36.3	506	10	Q9M143	Q9M143 arabidopsis
36	106	36.2	367	10	Q9C9T6	Q9C9T6 arabidopsis
37	106	36.2	425	5	P90990	P90990 caenorhabdi
38	106	36.2	524	10	Q9M411	Q9M411 arabidopsis
39	105	35.8	590	5	Q95QN6	Q95QN6 caenorhabdi
40	105	35.8	1256	5	Q9VG16	Q9VG16 drosophila
41	104.5	35.7	441	10	Q23446	Q23446 arabidopsis
42	104	35.5	351	10	Q9ZVU8	Q9ZVU8 arabidopsis
43	102.5	35.0	237	10	Q9S1J7	Q9S1J7 arabidopsis
44	102.5	35.0	451	11	Q9CXX8	Q9CXX8 mus musculu
45	102.5	35.0	482	5	Q9VD21	Q9VD21 drosophila

#### ALIGNMENTS

RESULT 1  
008854 PRELIMINARY; PRT; 470 AA.  
AC 008854;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MTRIP.  
GN TRAP OR MTRIP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97258620; PubMed=9104814;  
RA Lee S.Y., Lee S.Y., Choi Y.;  
RT "TRAF-interacting protein (TRIP): a novel component of the tumor  
necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes  
that inhibits TRAF2-mediated NF-kappaB activation.";  
RL J. Exp. Med. 185:1275-1285(1997).  
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: U77844; AAB52994.1; -  
DR MGI: 1096377; Traip.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
KW zinc-finger.  
SQ SEQUENCE 470 AA: 53191 MW: 00FD705B52645133 CRC64;

Query Match 100.0%; Score 293; DB 11; Length 470;  
Best Local Similarity 100.0%; Pred. No. 3.7e-31;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSLCTICSDFFDHSRDVAALHCGHTFHLLCCLIQMFETAPSRTPCQRIOVG 51  
DB 4 LSLCTICSDFFDHSRDVAALHCGHTFHLLCCLIQMFETAPSRTPCQRIOVG 54

```
RESULT 2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 223;
Pred. No. 1.5e-30;
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 51
:|||||
DB 5 ALCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 54

RESULT 3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC000310; AAH00310.1; -
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW ZINC-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 4; Length 469;
Pred. No. 3.2e-30;
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 51
:|||||
DB 5 ALCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 54

RESULT 4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;
```

```
GN TRAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 470;
Pred. No. 3.2e-30;
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 51
:|||||
DB 5 ALCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 54

RESULT 5
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 470;
Pred. No. 3.2e-30;
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 51
:|||||
DB 5 ALCTICSDPFDHSDVAIHGHTFHLQCLIQWETAPSRTPCPCRIQVG 54

RESULT 6
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;
```

DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
KW Zinc-finger.  
SQ SEQUENCE 469 AA; 53138 MW; 2D54ED04B64ABA64 CRC64;

Query Match 92.8%; Score 272; DB 4; Length 469;  
Best Local Similarity 96.0%; Pred. No. 2.4e-28;  
Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLCTISDFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 51  
:|||||  
DB 5 ALCTISDFDHSRDVAALHCGHTFHLQCLIQSFETAPSRTPCQCRIOVG 54

RESULT 6  
QYGN2 PRELIMINARY; PRT; 433 AA.  
AC QYGN2;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE TRAF INTERACTING PROTEIN.  
GN TRIP.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE-99148833; PubMed-10025966;  
RA Cottage A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M., Elgar G.;  
RT "Three receptor genes for plasmalogen related growth factors in the genome of the puffer fish Fugu rubripes.";  
RL FEBS Lett. 443:370-374(1999).  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: AJ010317; CAA09084.1; -;  
DR InterPro: IPR001841; Znf\_Tfng.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
KW Zinc-finger.  
SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

Query Match 83.3%; Score 244; DB 13; Length 433;  
Best Local Similarity 83.0%; Pred. No. 1.2e-24;  
Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 50  
:|||||  
DB 7 CTICSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 53

RESULT 7  
QYSSS5 PRELIMINARY; PRT; 435 AA.  
AC QYSSS5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE GH03577P.  
GN CG5140.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Plekoyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephyroidae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Y, CN BW SP;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunco J., Pacleb J., Paragas V., Park S., Phonanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Gelniker S.,  
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AY060610; AAL28158.1; -;  
SQ SEQUENCE 435 AA; 48455 MW; 0BFF0AC81DD9416E CRC64;

Query Match 43.7%; Score 128; DB 5; Length 435;  
Best Local Similarity 50.0%; Pred. No. 4.2e-09;  
Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCR 47  
:|||||  
DB 6 CVICAEILFGQADVEFATVCGHMFHNCINQWLDLR--SKTGPCR 47

RESULT 8  
QY8D7 PRELIMINARY; PRT; 455 AA.  
AC QY8D7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE CG5140 PROTEIN.  
GN CG5140.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Plekoyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephyroidae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Branton R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,  
RA Foslter A.C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,  
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Stykars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AEO03800; AAF57730.1; -  
 DR FlyBase: FBgn0034314; CGS140.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 455 AA; 50726 MW; BEA74F4CACE8FD5B CRC64;

Query Match 43.7%; Score 128; DB 5; Length 455;  
 Best Local Similarity 50.0%; Pred. No. 4.4e-09;  
 Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTICSDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 47  
 DB 6 CIVCAELFGADEVAFVATCGMHFNHCLNOMLDR-SKTCPOCR 47

RESULT 9  
 082372 PRELIMINARY; PRT; 310 AA.  
 AC 082372;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE AT2G29840 PROTEIN.  
 GN AT2G29840.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBL\_TaxID=3702;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlyum T.V.,  
 Beall C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 Cronin L.A., Shen M., VanAken S.E., Unagham L., Tallon L.J., Gill J.E.,  
 Adams M.D., Carrera A.J., Creasy T.H., Goodson H.M., Somerville C.R.,  
 Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 Salzberg S.L., Fraser C.M., Venter J.C.;  
 RA "Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*."  
 RT Nature 402:761-768(1999).  
 RL Nature 402:761-768(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AC005496; AAC35217.1; -  
 DR HSSP: P28990; ICHC.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 310 AA; 35390 MW; EEECL401152F5E2C CRC64;

Query Match 43.3%; Score 127; DB 10; Length 310;  
 Best Local Similarity 41.7%; Pred. No. 4e-09;  
 Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 LCTICSDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 50  
 DB 260 MCSICLFEFDGSRIVALPCGHEFDECAIKWET--NHDCPLCRFL 305

RESULT 10

075866 PRELIMINARY; PRT; 420 AA.  
 AC 075866;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE R1343.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBL\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lameudin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 Phan H., Velasco N., Do U., Regala W., Terry A., Barnes J.,  
 Dangnan L., Exler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 Attix C., Andreise T., Frankheim M., Amico-Keller G., Coetfield J.,  
 Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 Olsen A.S., Carrano A.V.;  
 RA "Sequence analysis of a 2.5 Mb region in 19p13.3."  
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AC005764; AAC62428.1; -  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR003137; PA.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF02225; PA; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWNM\_1.  
 KW Zinc-finger.  
 SQ SEQUENCE 420 AA; 45880 MW; 572731A8EBA97FCE CRC64;

Query Match 43.3%; Score 127; DB 4; Length 420;  
 Best Local Similarity 39.6%; Pred. No. 5.5e-09;  
 Matches 19; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 3 LCTICSDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 50  
 DB 299 LCAICLDEYEGDQLKLPCHSHYHCKIDPWFSQAPRRSCPYCKQSV 346

RESULT 11  
 09M908 PRELIMINARY; PRT; 325 AA.  
 AC 09M908;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE F6A14.12 PROTEIN.  
 GN F6A14.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBL\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
 Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,  
 Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,  
 Lueros S., Schwartz J., Shin P., Toriumi M., Vysotskaya V.S.,  
 Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;  
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AC011809; AAF27102.1; -  
 DR InterPro: IPR001664; IF.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.





```

Query Match          38.6%;   Score 113;   DB 10;   Length 386;
Best Local Similarity 36.0%;   Pred. No. 3.8e-07;
Matches 18; Conservative 9; Mismatches 21; Indels 2; Gaps 1
QY 1 LSLCTICDSFDHSDVAALHCGHFFHLOCLQLQWFFETASRRCPOCRIOY 50
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

KL Submitted (MAR-1

RA Mewes

RP SEQUENCE FROM N.A.  
RA Bevan M., Vandenbrouck M., Jallet C., Portetelle D., Honeisel J.,  
RA Mewes H.W., Mayer K., Schueller C.,  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE OF 65-344 FROM N.A.  
 RA Rose M., Hempel S., Ertlan K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Vandenbol M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AL022223; CA18230.1; -;  
 DR EMBL: AL161565; CAB79495.1; -;  
 DR InterPro: IPR001841; Znf\_r1ng.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Hypothetical protein; Zinc-finger.  
 SQ SEQUENCE 344 AA; 38720 MW; EB31D0BF5EDA700 CRC64;

Query Match 38.2%; Score 112; DB 10; Length 344;  
 Best Local Similarity 38.3%; Pred. No. 4.6e-07;  
 Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAALHCHTFHLQCLIQWFTAPSRTPCQCR 50  
 Db 229 CSICLDPDFDKGSEAKKPKHFKHRCIVPLWLEHSS--CPVCXYEL 273

RESULT 21  
 O944L9 PRELIMINARY; PRT; 368 AA.  
 AC O944L9;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AT1G17970/F2H15.16  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carlincl P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Yang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis cDNA clones."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF28290; AAL16122.1; -;  
 SQ SEQUENCE 368 AA; 41618 MW; 79AD48BD0790A08E CRC64;

Query Match 38.2%; Score 112; DB 10; Length 368;  
 Best Local Similarity 36.4%; Pred. No. 4.9e-07;  
 Matches 16; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAALHCHTFHLQCLIQWFTAPSRTPCQCR 47  
 Db 320 CSICDDEYERDEYELNGSHFVHCVKQWL--SRKNACPVC 361

RESULT 22  
 O9LMT3 PRELIMINARY; PRT; 383 AA.  
 ID O9LMT3

AC O9LMT3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE F2H15.19 PROTEIN.  
 GN F2H15.19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,  
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,  
 RA Altati H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,  
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,  
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,  
 RA Federspiel N.A., Theologis A.;  
 RT "The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AC034106; AAF97276.1; -;  
 DR InterPro: IPR001841; Znf\_r1ng.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 383 AA; 43262 MW; EE8ADE91FE0B224 CRC64;

Query Match 38.2%; Score 112; DB 10; Length 383;  
 Best Local Similarity 36.4%; Pred. No. 5.1e-07;  
 Matches 16; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAALHCHTFHLQCLIQWFTAPSRTPCQCR 47  
 Db 335 CSICDDEYERDEYELNGSHFVHCVKQWL--SRKNACPVC 376

RESULT 23  
 O9V9T8 PRELIMINARY; PRT; 621 AA.  
 AC O9V9T8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CG1937 PROTEIN.  
 GN CG1937.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Plamkuch C., Baldwin D.,  
 RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,







RESULT	30			
Q9FM98				
ID	Q9FM98	PRELIMINARY;	PRT:	396 AA.
AC	Q9FM98;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	GENOMIC DNA, CHROMOSOME 5, P1 CLONE:IMCD1.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons: core eudicots; Rosidae			
OC	eurosidis II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	MEDLINE=98290546; PubMed=9628582;			
RA	Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,			
RA	Tadaka S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. IV.			
RT	Sequence features of the regions of 1,456,315 bp covered by nineteen			
RT	physically assigned P1 and YAC clones."			
TL	DNA Res. 5:41-54(1998).			
CC	-1: SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL: AB009049; BAB11261.1; -			
DR	InterPro: IPR001841; Znf_ring.			
DR	Pfam: PF00097; zf-C3HC4; 1.			
DR	SMART: SM00184; RING; 1.			
DR	Zinc-finger.			
SC	SEQUENCE 396 AA; 44359 MW; 43059E73B44422FFB CRC64;			

[illegible]

```

RESULT 31
008109 ID Q08109 PRELIMINARY; PRT; 551 AA.
AC 008109;
DT 01-NOV-1996 (REMBLrel. 01, Created)
DT 01-NOV-1996 (REMBLrel. 01, last sequence update)
DT 01-DEC-2001 (REMBLrel. 19, last annotation update)
DE CHROMOSOME XV READING FRAME ORF YOL013C.
GN HRD1 OR YOL013C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NC1_Taxid=4932;
[1]
RN RA RP SEQUENCE FROM N.A.
RN RA RP Hughes B., Fohl T.M.;
RN RL RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN RA RP SEQUENCE FROM N.A.
RN RA RP MIPS;
RN RL RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; Z74755; CA99012.1; -.
DR SGD; S0005373; HRD1.
DR InterPro; IPR001841; znf_fing.
DR Pfam; PF00097; zf-C3HC4.1.
DR SMART; SM00184; RING; 1.
DR Zinc-finger.
KW SEQUENCE 551 AA; 63534 MW; CAA6341E7A94DB0B CRC64;

```

Query Match 36.5%; Score 107; DB 3; Length 551;

Best Local Similarity	37.3%;	Pred. No. 3.4e-06;
Matches	22;	Conservative 6; Mismatches 19; Indels 12; Gaps 2;

```
QY      2 SLCTICSDFFDHS-----RDVAALHCHTFHQCLLIOWETAPSRTCPCQRIV 50
        ::||| | : ||| ||| | :||| ||: |
Db    347 NICLICMDELHSPNQQTWKNKNNKKPKRLPCGHILHLSCLKMMMER--SQTCPICRLPV 403
```

RESULT	32			
090278				
ID	090278	PRELIMINARY;	PRT:	879 AA.
AC	090278;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RING FINGER PROTEIN (FRAGMENT).			
GN	ARKADIA.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Aurascopidae; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=21195971; Pubmed=11298452;			
RA	Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,			
RA	Swan D.;			
RT	"Induction of the mammalian node requires Arkadia function in the			
RT	extraembryonic lineages.";			
RL	Nature 410: 825-830(2001).			
DR	EMBL: AF329846; AAK38636.1; -.			
FT	NON_TER			
SO	SEQUENCE			
	879 AA;			
	95701 MW;			
	EC8564B2280E3264 CRC64;			

Query Match	36.5%;	Score 107;	DB 13;	length 879;
Best Local Similarity	38.3%;	Pred. No. 5.4e-06;		
Matches 18;	Conservative 7;	Mismatches 20;	Indels 2;	Gaps 1;

QY            4 CTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTPCQRIOV 50  
             |||| : ||| : ||| : ||| : ||| :  
Db          827 CTICSLIEGEDVRLPCMHLFHQCVDQLIT--NKKCPICRVDI 871

RESULT	33		
090277			
ID	Q90277	PRELIMINARY;	PRT; 923 AA.
AC	Q90277;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	RING FINGER-H2 PROTEIN (FRAGMENT).		
GN	ARKADIA.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;		
OC	Xenopodidae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21195971; PubMed-11298452;		
RA	Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,		
RA	Swan D.;		
RT	"Induction of the mammalian node requires Arkadia function in the		
RT	extraembryonic lineages.";		
RL	Nature 410:825-830(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Niederlaender C., Walsh J., Episkopou V., Jones M.;		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL, AF329847; AAK3637.1; -.		
NC	NON_TER		
QO	1	1	
	923 AA;	101298 MW	A93CBDA3E05787C8 CRC64;

Q SEQUENCE 923 AA; 101298 MW; A93CBDA3E05787C8 CRC64;



us-09-052-089a-6.rsp

0C Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae  
0C euroids II; Brassicales; Brassicaceae; Arabidopsis.

RP SEQUENCE FROM N.A.  
RA kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Shinn P.,  
RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.

RA Rowley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G., Davis R.W.  
RA redespisiel N.A., Theologis A., Ecker J.R.  
RT "Genomic sequence for *Arabidopsis thaliana* BAC F12M16 from chromosome  
BT I.";

```
CC -i SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC008007; AAF69531.1; -.
DR InterPro: IPR001841; ZnF_r1ng.
DR Pfam: PF000097; zf-C3HC4; 1.
```

KW Zinc-finger.  
 SQ SEQUENCE 524 AA; 58471 MW; CFFC6AB4E39BD6F CRC64;

4 CTTCSDFDHSRDAVAIHCGHTFPHLOCLIQWFETAPSRTPCQCR 47  
Best Local Similarity 36.4%; Pred. NO. 4.4e-06;  
Matches 16; Conservative 8; Mismatches 18; Indels 2; Caps

```
Db      472 CTTCQSEFNKEKIATLDCGHEHYAECLEKWL--IVANVCPICK 513
RESULT 39
```

ID	Q95QN6	PRELIMINARY	PRT	590 AA.
AC	Q95QN6			
DT	01-DEC-2001	(TREMblrel. 19, Created)		
DT	01-DEC-2001	(TREMblrel. 19, Last sequence update)		

DE HYPOTHETICAL 67.4 KDA PROTEIN.  
GN EED8.16.  
OS *Caenorhabditis elegans*.  
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae;

OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
CC	STRAIN-BRISTOL N2;

RA	None;
RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for
RT	Investigating biology. The <i>C. elegans</i> Sequencing Consortium.,"
TL	Science 283:2012-2018(1998).

RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Chisoe S.;

TT "The sequence of C. elegans cosmid EEPD8";

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL NZ;  
RA Waterston R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL: U23484; AAK93844.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 590 AA: 67414 MW: 56EA3FEEDBD7D9CE8 CRC64:

Query Match 35.8%; Score 105; DB 5; Length 590;  
 Best Local Similarity 44.7%; Pred. No. 6.8e-06;  
 Matches 21; Conservative 5; Mismatches 15; Indels 6; Gaps

OY 1 LSLCTCSDFPDHSDVAAIHCGTFPHLOCLIQWFTAPSRPCPOCR 47  
 DB 257 LPTCAVCLERNDDS--VLATICNHSFARCLEQWAD-----NTCVCVR 297  
 RESULT 40  
 OYVGI6 PRELIMINARY; PRT; 1256 AA.  
 AC OYVGI6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CG6923 PROTEIN (L222771p).  
 GS CG6923.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL, AE003692; AAF54693.1; -;  
 DR EMBL, AY058520; AAL13749.1; -;

DR HSSP; P28990; ICHC.  
 DR FlyBase; FBgn0037944; CG6923.  
 DR InterPro; IPR001841; znf\_ring.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 KW zinc-finger.  
 SQ SEQUENCE 1256 AA; 138666 MW; 17FA760165507EAE CRC64;  
 OY 4 CTICSDFFDHSRDVAAIHCGTFPHLOCLIQWFTAPSRPCPOCR 50  
 DB 1187 CAICLNLFEIENEYRRLLPCMHLPHTDCVDMVLT--NKHCPCRVDI 1231  
 Query Match 35.8%; Score 105; DB 5; Length 1256;  
 Best Local Similarity 36.2%; Pred. No. 1.4e-05;  
 Matches 17; Conservative 9; Mismatches 19; Indels 2; Gaps 1;

Search completed: September 4, 2002, 16:16:09  
 Job time: 1493 sec



**THIS PAGE BLANK (USPTO)**